

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 22, 2005, 23:34:02 ; Search time 2378.54 Seconds  
(without alignments)  
4701.242 Million cell updates/sec

Title: US-10-614-282-1

Perfect score: 239

Sequence: 1 atcagtcacgacttggttaag.....tgtggttccggtggacaat 239

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hc:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gss1:\*  
10: gb\_gss2:\*  
11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	239	100.0	510	3	B1375946
2	145.4	60.8	379	7	C0306026
3	37.2	15.6	1138	3	B0144508
4	35.6	14.9	162	5	BW068571
5	35.2	14.7	625	10	CL579846
6	35.2	14.7	712	10	CL574949
7	35	14.6	496	2	BF024030
8	34.8	14.6	625	6	CD648340
9	34.6	14.5	563	9	A2581975
10	34.4	14.4	698	8	DN983220
11	34	14.2	670	11	LBFA025H06
12	34	14.2	670	11	LBFA025H09
13	33.8	14.1	507	10	BX137891
14	33.6	14.1	638	9	A2983355
15	33.6	14.1	833	10	CZ712792
16	33.4	14.0	845	6	CF813122
17	33.4	14.0	849	7	C0014533
18	33.4	14.0	855	6	CF818084
19	33.4	14.0	1026	4	AF227817
20	33.2	13.9	537	5	BQ743358
21	33.2	13.9	557	3	BJ645949
22	33	13.8	273	10	CZ915578

23	32.8	13.7	349	5	BU578178
24	32.8	13.7	438	1	AW133037
25	32.8	13.7	443	2	BE803253
26	32.8	13.7	446	2	BG725287
27	32.8	13.7	642	7	CV504660
28	32.8	13.7	773	9	BH465834
29	32.8	13.7	955	5	BU901940
c	30	32.6	624	10	BX139003
31	32.6	13.6	827	7	CO035667
32	32.6	13.6	852	6	CD649081
33	32.6	13.6	866	7	CO031945
34	32.6	13.6	895	6	CD048532
35	32.4	13.6	607	10	CW060437
36	32.4	13.6	616	7	CK571307
37	32.4	13.6	680	10	CW463755
c	38	32.4	691	10	CW229198
39	32.4	13.6	835	10	CW987242
40	32.2	13.5	483	7	CN242214
c	41	32.2	565	5	BY492451
c	42	32.2	648	10	CE691717
c	43	32.2	664	2	BE941338
44	32	13.4	134	1	AU077131
c	45	32	457	1	AJ791110

## ALIGNMENTS

RESULT 1  
B1375946  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES

B1375946 510 bp mRNA linear EST 16-JAN-2004  
RE63854.Sprime RE Drosophila melanogaster normalized Embryo pFlc-1  
Drosophila melanogaster cDNA clone RE63854 5, mRNA sequence.

B1375946  
GI:15071974  
EST.  
Drosophila melanogaster (fruit fly)  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 510)  
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B.,  
Carlson, J., Chavez, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E.,  
George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G.,  
Misra, S., Mungall, C.J., Nunoo, J., Pacleb, J., Pargass, V., Park, S.,  
Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and  
Rubin, G.M.  
BDGP/HMI RE Drosophila EST Project  
Unpublished (2001)  
Other ESTs: RE63854.3prime  
Contact: Stapleton, M.  
BDGP  
Lawrence Berkeley National Lab  
One Cyclotron Rd, Berkeley, CA 94720, USA  
Fax: 510 486 6798  
Email: [http://www.fruitfly.org/EST\\_est@fruitfly.berkeley.edu](http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu)  
hit genomic AB003674: arm:3R [2306679,2604706]  
estimated-cyto:83F1-84A5: 05/16/2001  
Plate: RE.638 row: E column: 6  
High quality sequence stop: 453.  
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/mol\_type="mRNA"  
/db\_xref="taxon:7227"  
/clone="RE63854"  
/sex="male and female"  
/dev\_stage="0-24 hours mixed stage embryonic"  
/lab\_hosts="DHS-alpha Tona"  
/clone\_lib="RE Drosophila melanogaster normalized Embryo  
pFlc-1"  
/note="Organ: embryo; Vector: pFlc1; Site\_1: XhoI; Site\_2: